# PCT

## INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

| Applicant's or agent's file reference<br>X-11600 | FOR FURTHER ACTION | see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below. | |
|---|---|---|---|
| International application No.<br>PCT/US 00/ 06707 | International filing date *(day/month/year)*<br>09/05/2000 | | (Earliest) Priority Date *(day/month/year)*<br>11/05/1999 |

| Applicant |
|---|
| ELI LILLY AND COMPANY |

This International Search Report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This International Search Report consists of a total of ___5___ sheets.

[X] It is also accompanied by a copy of each prior art document cited in this report.

1. **Basis of the report**

   a. With regard to the **language**, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.

   [ ] the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).

   b. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international search was carried out on the basis of the sequence listing :

   [ ] contained in the international application in written form.

   [ ] filed together with the international application in computer readable form.

   [X] furnished subsequently to this Authority in written form.

   [X] furnished subsequently to this Authority in computer readble form.

   [X] the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

   [X] the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished

2. [X] **Certain claims were found unsearchable** (See Box I).

3. [ ] **Unity of invention is lacking** (see Box II).

4. With regard to the **title**,

   [X] the text is approved as submitted by the applicant.

   [ ] the text has been established by this Authority to read as follows:

5. With regard to the **abstract**,

   [X] the text is approved as submitted by the applicant.

   [ ] the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the **drawings** to be published with the abstract is Figure No. _____

   [ ] as suggested by the applicant.

   [ ] because the applicant failed to suggest a figure.

   [ ] because this figure better characterizes the invention.

   [ ] None of the figures.

**FURTHER INFORMATION CONTINUED FROM     PCT/ISA/ 210**

Continuation of Box I.2

Claims Nos.:   21,22

Claims 21 and 22 refer to an antagonist/inhibitor of the polypeptide
without giving a true technical
characterization. Moreover, no such compunds are defined in the
application. In consequence, the
scope of said claims is ambigous and vague, and their subject-matter is
not sufficiently disclosed
and supported (Art. 6 PCT). No search could be carried out for such
purely speculative claims whose wording is, in fact, a mere recitation of
the result to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of
claims, relating to inventions in respect of which no international
search report has been established need not be the subject of an
international preliminary examination (Rule 66.1(e) PCT). The applicant
is advised that the EPO policy when acting as an International
Preliminary Examining Authority is normally not to carry out a
preliminary examination on matter which has not been searched. This is
the case irrespective of whether or not the claims are amended following
receipt of the search report or during any Chapter II procedure.

# INTERNATIONAL SEARCH REPORT

## A. CLASSIFICATION OF SUBJECT MATTER
IPC 7   C07K14/47   C12N15/57   C12N9/64   C12N5/10   C12N5/16
A61P25/28

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7   C12N   C07K   A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

STRAND, EMBL, GENSEQ, EPO-Internal

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X | DATABASE GENEMBL 'Online! 6 June 1996 (1996-06-06) HILLIER ET AL.: "yx480g8.r1 soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:265022 5' similar to contains Alu repetitive element" XP002148339 Accesion number N30496 --- | 1-16 |
| X | WO 96 40885 A (MCCONLOGUE LISA C ;KEIM PAMELA S (US); SINHA SUKANTO (US); TAN HUA) 19 December 1996 (1996-12-19) page 22, line 20 -page 23, line 2 page 41, line 20 -page 48, line 34 claims 23-41; table 3 --- -/-- | 17 |

[X] Further documents are listed in the continuation of box C.      [X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

| Date of the actual completion of the international search | Date of mailing of the international search report |
|---|---|
| 4 October 2000 | 17/10/2000 |

| Name and mailing address of the ISA | Authorized officer |
|---|---|
| European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31–70) 340–2040, Tx. 31 651 epo nl, Fax: (+31–70) 340–3016 | ALCONADA RODRIG.., A |

Form PCT/ISA/210 (second sheet) (July 1992)

Internati Application No

PCT/ 00/06707

| Category ° | Citation of document, with indication,where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|

**C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT**

| X | EP 0 653 154 A (HOECHST JAPAN)<br>17 May 1995 (1995-05-17)<br>page 5, line 13-21<br>claim 10 | 19 |
|---|---|---|
| A | DATABASE SWISSPROT 'Online!<br>1 June 1998 (1998-06-01)<br>HUSAINI ET AL.: "Bos taurus butyrophilin<br>fragment"<br>XP002148340<br>Accession No. 046535 | 1-16 |
| P,X | WO 99 46281 A (BAKER KEVIN P ;CHEN JIAN<br>(US); GENENTECH INC (US); GURNEY AUSTIN ()<br>16 September 1999 (1999-09-16)<br>page 12, line 24-35<br>page 60, line 10-29<br>page 128, line 15-22<br>page 149, line 30-33<br>page 151, line 22-30<br>page 159, line 17-19 | 1-16 |

3

| Patent document cited in search report | | Publication date | Patent family member(s) | | Publication date |
|---|---|---|---|---|---|
| WO 9640885 | A | 19-12-1996 | US | 5744346 A | 28-04-1998 |
| | | | AU | 6383396 A | 30-12-1996 |
| | | | EP | 0871720 A | 21-10-1998 |
| | | | JP | 11507538 T | 06-07-1999 |
| | | | US | 5942400 A | 24-08-1999 |
| EP 0653154 | A | 17-05-1995 | JP | 7132033 A | 23-05-1995 |
| | | | CA | 2135595 A | 13-05-1995 |
| | | | US | 6037521 A | 14-03-2000 |
| WO 9946281 | A | 16-09-1999 | AU | 3072199 A | 27-09-1999 |
| | | | AU | 3075099 A | 11-10-1999 |
| | | | WO | 9947677 A | 23-09-1999 |
| | | | AU | 1532499 A | 15-06-1999 |
| | | | EP | 1032667 A | 06-09-2000 |
| | | | WO | 9927098 A | 03-06-1999 |
| | | | AU | 3757099 A | 08-11-1999 |
| | | | WO | 9954467 A | 28-10-1999 |
| | | | AU | 1070399 A | 10-05-1999 |
| | | | EP | 1025227 A | 09-08-2000 |
| | | | WO | 9920756 A | 29-04-1999 |

# PATENT COOPERATION TREATY

by fax and post

RECEIVED

PCT

AUG 0 3 2001

ELI LILLY & COMPANY
PATENT DIVISION

To:

HUNTER, Frederick D.
ELI LILLY AND COMPANY
Lilly Corporate Center
Indianapolis, Indiana 46285
ETATS-UNIS D'AMERIQUE

FAX NO: (317) 276-3861

**NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL PRELIMINARY EXAMINATION REPORT**

(PCT Rule 71.1)

| Date of mailing (day/month/year) | 27.07.2001 |
|---|---|

| Applicant's or agent's file reference | |
|---|---|
| X-11600 | **IMPORTANT NOTIFICATION** |

| International application No. | International filing date (day/month/year) | Priority date (day/month/year) |
|---|---|---|
| PCT/US00/06707 | 09/05/2000 | 11/05/1999 |

| Applicant |
|---|
| ELI LILLY AND COMPANY et al. |

1. The applicant is hereby notified that this International Preliminary Examining Authority transmits herewith the international preliminary examination report and its annexes, if any, established on the international application.

2. A copy of the report and its annexes, if any, is being transmitted to the International Bureau for communication to all the elected Offices.

3. Where required by any of the elected Offices, the International Bureau will prepare an English translation of the report (but not of any annexes) and will transmit such translation to those Offices.

4. **REMINDER**

   The applicant must enter the national phase before each elected Office by performing certain acts (filing translations and paying national fees) within 30 months from the priority date (or later in some Offices) (Article 39(1)) (see also the reminder sent by the International Bureau with Form PCT/IB/301).

   Where a translation of the international application must be furnished to an elected Office, that translation must contain a translation of any annexes to the international preliminary examination report. It is the applicant's responsibility to prepare and furnish such translation directly to each elected Office concerned.

   For further details on the applicable time limits and requirements of the elected Offices, see Volume II of the PCT Applicant's Guide.

| Name and mailing address of the IPEA/ | Authorized officer |
|---|---|
| European Patent Office D-80298 Munich Tel. +49 89 2399 - 0  Tx· 523656 epmu d Fax: +49 89 2399 - 4465 | Büchler, S Tel.+49 89 2399-8090 |

Form PCT/IPEA/416 (July 1992)

# PATENT COOPERATION TREATY

# PCT

## INTERNATIONAL PRELIMINARY EXAMINATION REPORT

### (PCT Article 36 and Rule 70)

| Applicant's or agent's file reference<br><br>X-11600 | **FOR FURTHER ACTION** | See Notification of Transmittal of International<br>Preliminary Examination Report (Form PCT/IPEA/416) |
|---|---|---|
| International application No.<br><br>PCT/US00/06707 | International filing date *(day/month/year)*<br><br>09/05/2000 | Priority date *(day/month/year)*<br><br>11/05/1999 |

International Patent Classification (IPC) or national classification and IPC
C07K14/47

Applicant

ELI LILLY AND COMPANY  et al.

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.

2. This REPORT consists of a total of  6 sheets, including this cover sheet.

   ☐ This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

   These annexes consist of a total of  sheets.

3. This report contains indications relating to the following items:

   I   ☒ Basis of the report
   II  ☐ Priority
   III ☒ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
   IV  ☐ Lack of unity of invention
   V   ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations suporting such statement
   VI  ☐ Certain  documents cited
   VII ☐ Certain defects in the international application
   VIII ☒ Certain observations on the international application

| Date of submission of the demand<br><br>13/11/2000 | Date of completion of this report<br><br>27.07.2001 |
|---|---|
| Name and mailing address of the international preliminary examining authority:<br><br>European Patent Office<br>D-80298 Munich<br>Tel. +49 89 2399 - 0  Tx: 523656 epmu d<br>Fax: +49 89 2399 - 4465 | Authorized officer<br><br>Loubradou, G<br><br>Telephone No. +49 89 2399 8543 |

Form PCT/IPEA/409 (cover sheet) (January 1994)

## I. Basis of the report

1. With regard to the **elements** of the international application *(Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17))*:
   **Description, pages:**

   1-72                     as originally filed


   **Claims, No.:**

   1-22                     as originally filed


   **Sequence listing part of the description, pages:**

   1-11, filed with the letter of 07.08.2000

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

   These elements were available or furnished to this Authority in the following language:    , which is:

   ☐   the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).

   ☐   the language of publication of the international application (under Rule 48.3(b)).

   ☐   the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

   ☐   contained in the international application in written form.

   ☐   filed together with the international application in computer readable form.

   ☒   furnished subsequently to this Authority in written form.

   ☒   furnished subsequently to this Authority in computer readable form.

   ☒   The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

   ☒   The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

   ☐   the description,        pages:

   ☐   the claims,             Nos.:

   ☐   the drawings,           sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

   *(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)*

6. Additional observations, if necessary:

## III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

1. The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

   ☐   the entire international application.

   ☒   claims Nos. 21, 22.

   because:

   ☐   the said international application, or the said claims Nos.  relate to the following subject matter which does not require an international preliminary examination (*specify*):

   ☐   the description, claims or drawings (*indicate particular elements below*) or said claims Nos.  are so unclear that no meaningful opinion could be formed (*specify*):

   ☐   the claims, or said claims Nos.  are so inadequately supported by the description that no meaningful opinion could be formed.

   ☒   no international search report has been established for the said claims Nos. 21, 22.

2. A meaningful international preliminary examination cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

   ☐   the written form has not been furnished or does not comply with the standard.

   ☐   the computer readable form has not been furnished or does not comply with the standard.

## V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

   Novelty (N)     Yes:   Claims   2, 3, 5-16, 18-20
                   No:    Claims   1, 4, 17

   Inventive step (IS)   Yes:   Claims   2, 3, 5-16, 18-20

|  | No: | Claims | 1, 4, 17 |
|---|---|---|---|
| Industrial applicability (IA) | Yes: | Claims | 1-20 |
|  | No: | Claims |  |

2. Citations and explanations
   **see separate sheet**


**VIII. Certain observations on the international application**

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:
**see separate sheet**

Reference is made to the following documents:

> D1: WO 96 40885 A (MCCONLOGUE LISA C ;KEIM PAMELA S (US);
> SINHA SUKANTO (US); TAN HUA) 19 December 1996 (1996-12-19)

> D2: DATABASE GENEMBL [Online] 6 June 1996 (1996-06-06) HILLIER
> ET AL.: 'yx480g8.r1 soares melanocyte 2NbHM Homo sapiens cDNA
> clone IMAGE:265022 5' similar to contains Alu repetitive element'
> XP002148339

### Re Item V

Reasoned statement under Rule 66.2(a)(ii) with regard to novelty, inventive step or
industrial applicability; citations and explanations supporting such statement

1.  D1 discloses the purification of a β-secretase protein. The starting material of D1
    is identical to the starting material the present application, the β-secretase activity
    assay are similar and several purification steps are shared with the purification of
    the present application (see D1 pages 28 to 30 paragraph entitled "Purification
    and characterisation of β-secretase"). The partial sequences obtained from the
    protein of D1 seem not to be present in SEQ ID NO:2 or SEQ ID NO:4 of the
    present application therefore the proteins having said SEQ IDs appear to be novel
    with regard to the protein of D1. However the present claim 1 is drafted so broadly
    that its scope encompasses any protein being a "functional equivalent" of the
    proteins having said SEQ IDs without any limitation in sequence requirement (see
    also paragraph 5.). Therefore D1 is prejudicial for the novelty of claim 1.

2.  The attention of the applicant is drawn to the fact that the SEQ ID NO:2 comprises
    a stretch of 27 undetermined amino acids. This implies that the statement "a
    fragment of at least 6 continuous amino acids thereof" in claim 1 encompasses all
    the fragments of the prior art having between 6 and 27 amino acids (Article 33.2
    PCT).
    In addition, the fragments "of at least 6 continuous amino acids" of claim 1 do not

appear to solve any technical problem. Consequently said fragments are merely considered as an arbitrary selection among all possible fragments of at least 6 amino acids. Therefore even in absence of undetermined amino acids in the SEQ ID NO: 2, claim 1 would be considered as lacking an inventive step (Article 33.3 PCT).

3.  D2 discloses a sequence which is 97% identical to the sequence of SEQ ID NO:3 in 485 nucleotide overlap. A fragment having said sequence of D2 inherently selectively hybridises with the sequence of SEQ ID NO:3. D2 is therefore prejudicial for the novelty of claim 4 f).

4.  D1 (page 41 line 16 to page 44 line 17) describes a β-secretase inhibitor assay utilizing purified β-secretase which anticipates claim 17 of the present application (Article 33.2 PCT).

## Re Item VIII
Certain observations on the international application

5.  The terms "functional equivalent" used in claim 1 are vague and unclear and leave the reader in doubt as to the meaning of the technical features to which they refer, thereby rendering the definition of the subject-matter of said claim unclear (Article 6 PCT).

6.  Claim 19 does not meet the criteria of Article 6 PCT. The present application does not provide a β-secretase different from the protein having the sequences shown in SEQ IDs No: 2 and 4. Therefore claim 19 is not supported by the description over its entire scope.

7.  The same enzyme should not be given different names in the claims (Article 6 PCT). In claims 1, 4 and 11 the enzyme of the present application is named "an amyloid precursor protein protease" and in claims 17 to 20 said enzyme is referred to as a "β-secretase".

IN THE UNITED STATES RECEIVING OFFICE (USRO)

Applicant(s):  Gerald Wayne Becker
International Application No.:   PCT/US00/06707
Filed:  05/09/2000 (05.09.00)
Invention:  AMYLOID PRECURSOR PROTEIN PROTEASE AND RELATED NUCLEIC ACID
COMPOUNDS
Lilly Reference:   X-11600
Earliest Priority Date:  05/11/1999 (05.11.1999)

## Certificate Under 37 C.F.R. § 1.10

Attention:  DO/EO
Box PCT
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir/Madam:

"Express Mail" mailing label number:   ___EL559725839US___
Date of Deposit:  ___October 30, 2001___

I hereby certify that the following attached paper or fee

Transmittal Letter to the United States Designated/Elected Office (US) concerning a filing under
35 U.S.C. 371 of the International Application identified above is being deposited with the United
States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. 1.10 on
the date indicated above and is addressed to the Assistant Commissioner for Patents,
Washington, D.C. 20231.

___Olga M Franz___
(Typed or printed name of person mailing paper)

___Olga M Franz___
(Signature of person mailing paper or fee)

# PATENT COOPERATION TREATY

# PCT

REC'D 3 1 JUL 2001

WIPO

## INTERNATIONAL PRELIMINARY EXAMINATION REPORT

## (PCT Article 36 and Rule 70)

*14*

| Applicant's or agent's file reference<br>X-11600 | **FOR FURTHER ACTION** | See Notification of Transmittal of International<br>Preliminary Examination Report (Form PCT/IPEA/416) |
|---|---|---|
| International application No.<br>PCT/US00/06707 | International filing date *(day/month/year)*<br>09/05/2000 | Priority date *(day/month/year)*<br>11/05/1999 |

International Patent Classification (IPC) or national classification and IPC
C07K14/47

Applicant

ELI LILLY AND COMPANY  et al.

1.  This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.

2.  This REPORT consists of a total of  6 sheets, including this cover sheet.

    ☐  This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

    These annexes consist of a total of  sheets.

3.  This report contains indications relating to the following items:

    I    ☒  Basis of the report
    II   ☐  Priority
    III  ☒  Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
    IV   ☐  Lack of unity of invention
    V    ☒  Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations suporting such statement
    VI   ☐  Certain  documents cited
    VII  ☐  Certain defects in the international application
    VIII ☒  Certain observations on the international application

| Date of submission of the demand<br><br>13/11/2000 | Date of completion of this report<br><br>27.07.2001 |
|---|---|
| Name and mailing address of the international<br>preliminary examining authority:<br><br>European Patent Office<br>D-80298 Munich<br>Tel. +49 89 2399 - 0  Tx: 523656 epmu d<br>Fax: +49 89 2399 - 4465 | Authorized officer<br><br>Loubradou, G<br><br>Telephone No. +49 89 2399 8543 |

Form PCT/IPEA/409 (cover sheet) (January 1994)

### I.  Basis of the report

1. With regard to the **elements** of the international application *(Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17))*:
**Description, pages:**

    1-72                          as originally filed


    **Claims, No.:**

    1-22                          as originally filed


    **Sequence listing part of the description, pages:**

    1-11, filed with the letter of 07.08.2000

2. With regard to the **language,** all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

    These elements were available or furnished to this Authority in the following language:    , which is:

    ☐   the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
    ☐   the language of publication of the international application (under Rule 48.3(b)).
    ☐   the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

    ☐   contained in the international application in written form.
    ☐   filed together with the international application in computer readable form.
    ☒   furnished subsequently to this Authority in written form.
    ☒   furnished subsequently to this Authority in computer readable form.
    ☒   The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
    ☒   The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

    ☐   the description,       pages:
    ☐   the claims,          Nos.:
    ☐   the drawings,        sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

*(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)*

6. Additional observations, if necessary:

## III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

1. The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

   ☐ the entire international application.

   ☒ claims Nos. 21, 22.

because:

   ☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):

   ☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):

   ☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.

   ☒ no international search report has been established for the said claims Nos. 21, 22.

2. A meaningful international preliminary examination cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

   ☐ the written form has not been furnished or does not comply with the standard.
   ☐ the computer readable form has not been furnished or does not comply with the standard.

## V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

| | | | |
|---|---|---|---|
| Novelty (N) | Yes: | Claims | 2, 3, 5-16, 18-20 |
| | No: | Claims | 1, 4, 17 |
| Inventive step (IS) | Yes: | Claims | 2, 3, 5-16, 18-20 |

|  | No: | Claims | 1, 4, 17 |
| Industrial applicability (IA) | Yes: | Claims | 1-20 |
|  | No: | Claims |  |

2.  Citations and explanations
    **see separate sheet**

**VIII. Certain observations on the international application**

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:
**see separate sheet**

Reference is made to the following documents:

D1:  WO 96 40885 A (MCCONLOGUE LISA C ;KEIM PAMELA S (US);
SINHA SUKANTO (US); TAN HUA) 19 December 1996 (1996-12-19)

D2:  DATABASE  GENEMBL [Online] 6 June 1996 (1996-06-06) HILLIER
ET AL.: 'yx480g8.r1 soares melanocyte 2NbHM Homo sapiens cDNA
clone IMAGE:265022 5' similar to contains Alu repetitive element'
XP002148339

## Re Item V

Reasoned statement under Rule 66.2(a)(ii) with regard to novelty, inventive step or
industrial applicability; citations and explanations supporting such statement

1.    D1 discloses the purification of a β-secretase protein. The starting material of D1
is identical to the starting material the present application, the β-secretase activity
assay are similar and several purification steps are shared with the purification of
the present application (see D1 pages 28 to 30 paragraph entitled "Purification
and characterisation of β-secretase"). The partial sequences obtained from the
protein of D1 seem not to be present in SEQ ID NO:2 or SEQ ID NO:4 of the
present application therefore the proteins having said SEQ IDs appear to be novel
with regard to the protein of D1. However the present claim 1 is drafted so broadly
that its scope encompasses any protein being a "functional equivalent" of the
proteins having said SEQ IDs without any limitation in sequence requirement (see
also paragraph 5.). Therefore D1 is prejudicial for the novelty of claim 1.

2.    The attention of the applicant is drawn to the fact that the SEQ ID NO:2 comprises
a stretch of 27 undetermined amino acids.  This implies that the statement "a
fragment of at least 6 continuous amino acids thereof" in claim 1 encompasses all
the fragments of the prior art having between 6 and 27 amino acids (Article 33.2
PCT).
In addition, the fragments "of at least 6 continuous amino acids" of claim 1 do not

appear to solve any technical problem. Consequently said fragments are merely considered as an arbitrary selection among all possible fragments of at least 6 amino acids. Therefore even in absence of undetermined amino acids in the SEQ ID NO: 2, claim 1 would  be considered as lacking an inventive step (Article 33.3 PCT).

3.　D2 discloses a sequence which is 97% identical to the sequence of SEQ ID NO:3 in 485 nucleotide overlap. A fragment having said sequence of D2 inherently selectively hybridises with the sequence of SEQ ID NO:3. D2 is therefore prejudicial for the novelty of claim 4 f).

4.　D1 (page 41 line 16 to page 44 line 17) describes a β-secretase inhibitor assay utilizing purified β-secretase which anticipates claim 17 of the present application (Article 33.2 PCT).

**Re Item VIII**
Certain observations on the international application

5.　The terms "functional equivalent" used in claim 1 are vague and unclear and leave the reader in doubt as to the meaning of the technical features to which they refer, thereby rendering the definition of the subject-matter of said claim unclear (Article 6 PCT).

6.　Claim 19 does not meet the criteria of Article 6 PCT. The present application does not provide a β-secretase different from the protein having the sequences shown in SEQ IDs No: 2 and 4. Therefore claim 19 is not supported by the description over its entire scope.

7.　The same enzyme should not be given different names in the claims (Article 6 PCT). In claims 1, 4 and 11 the enzyme of the present application is named "an amyloid precursor protein protease" and in claims 17 to 20 said enzyme is referred to as a "β-secretase".

| (51) International Patent Classification 7 : C07K 14/47, C12N 15/57, 9/64, 5/10, 5/16, A61P 25/28 | A1 | (11) International Publication Number: WO 00/68266 |
|---|---|---|
| | | (43) International Publication Date: 16 November 2000 (16.11.00) |

(21) International Application Number: PCT/US00/06707

(22) International Filing Date: 9 May 2000 (09.05.00)

(30) Priority Data:
60/133,423    11 May 1999 (11.05.99)    US

(71) Applicant (for all designated States except US): ELI LILLY AND COMPANY [US/US]; Lilly Corporate Center, Indianapolis, IN 46285 (US).

(72) Inventors; and
(75) Inventors/Applicants (for US only): BECKER, Gerald, Wayne [US/US]; 10815 East 121st Street, Fishers, IN 46038 (US). HALE, John, Edward [US/US]; 7644 Forest Drive, Fishers, IN 46038 (US). HEATH, William, Francis, Jr. [US/US]; 11214 Tuffton Street, Fishers, IN 46038 (US). JOHNSTONE, Edward, Marion [US/US]; 5129 East 69th Street, Indianapolis, IN 46220 (US). LITTLE, Sheila, Parks [US/US]; 4480 North Meridian Street, Indianapolis, IN 46208 (US). TU, Yuan [US/US]; 10848 Madeline Court, Fishers, IN 46038 (US). YEH, Wu–Kuang [US/US]; 720 Primrose Court, Greenwood, IN 46142 (US). YIN, Tinggui [CN/US]; 409 Mari Way, Carmel, IN 46032 (US).

(74) Agents: WILSON, Alexander et al.; Eli Lilly and Company, Lilly Corporate Center, Indianapolis, IN 46285 (US).

(81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published
*With international search report.*
*Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.*

(54) Title: AMYLOID PRECURSOR PROTEIN PROTEASE AND RELATED NUCLEIC ACID COMPOUNDS

(57) Abstract

This present invention provides an amyloid precursor protein protease and related nucleic acid compounds thereof. The invention also provides compositions, expression vectors, and transfected host cells as well as assays and methods of use. The compounds of the present invention will further characterize Alzheimer's Disease and other neurodegenerative disease states.

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC 7 C07K14/47 C12N15/57 C12N9/64 C12N5/10 C12N5/16
A61P25/28

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

STRAND, EMBL, GENSEQ, EPO-Internal

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

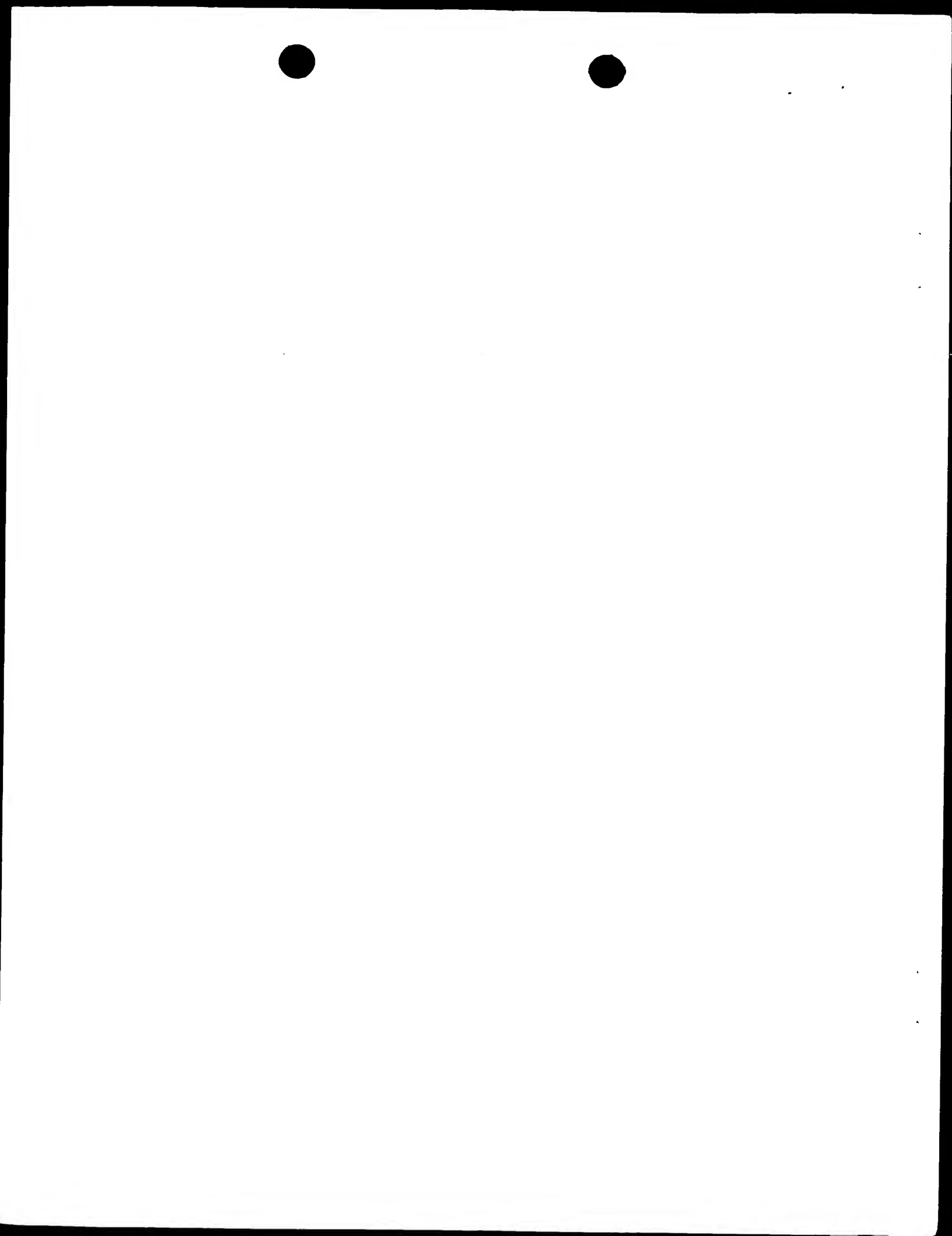| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X | DATABASE GENEMBL 'Online! 6 June 1996 (1996-06-06) HILLIER ET AL.: "yx480g8.r1 soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:265022 5' similar to contains Alu repetitive element" XP002148339 Accesion number N30496 | 1-16 |
| X | WO 96 40885 A (MCCONLOGUE LISA C ;KEIM PAMELA S (US); SINHA SUKANTO (US); TAN HUA) 19 December 1996 (1996-12-19) page 22, line 20 -page 23, line 2 page 41, line 20 -page 48, line 34 claims 23-41; table 3 | 17 |

-/—

| X | Further documents are listed in the continuation of box C. |
|---|---|

| X | Patent family members are listed in annex. |
|---|---|

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

| Date of the actual completion of the international search | Date of mailing of the international search report |
|---|---|
| 4 October 2000 | 17/10/2000 |

| Name and mailing address of the ISA | Authorized officer |
|---|---|
| European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016 | ALCONADA RODRIG.., A |

3

Form PCT/ISA/210 (second sheet) (July 1992)

International Application No

PCT/US 00/06707

**C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT**

| Category ° | Citation of document, with indication,where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X | EP 0 653 154 A (HOECHST JAPAN)<br>17 May 1995 (1995-05-17)<br>page 5, line 13-21<br>claim 10 | 19 |
| A | DATABASE SWISSPROT 'Online!<br>1 June 1998 (1998-06-01)<br>HUSAINI ET AL.: "Bos taurus butyrophilin fragment"<br>XP002148340<br>Accession No. 046535 | 1-16 |
| P,X | WO 99 46281 A (BAKER KEVIN P ;CHEN JIAN (US); GENENTECH INC (US); GURNEY AUSTIN ())<br>16 September 1999 (1999-09-16)<br>page 12, line 24-35<br>page 60, line 10-29<br>page 128, line 15-22<br>page 149, line 30-33<br>page 151, line 22-30<br>page 159, line 17-19 | 1-16 |

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**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

Continuation of Box I.2

Claims Nos.: 21,22

Claims 21 and 22 refer to an antagonist/inhibitor of the polypeptide
without giving a true technical
characterization. Moreover, no such compunds are defined in the
application. In consequence, the
scope of said claims is ambigous and vague, and their subject-matter is
not sufficiently disclosed
and supported (Art. 6 PCT). No search could be carried out for such
purely speculative claims whose wording is, in fact, a mere recitation of
the result to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of
claims, relating to inventions in respect of which no international
search report has been established need not be the subject of an
international preliminary examination (Rule 66.1(e) PCT). The applicant
is advised that the EPO policy when acting as an International
Preliminary Examining Authority is normally not to carry out a
preliminary examination on matter which has not been searched. This is
the case irrespective of whether or not the claims are amended following
receipt of the search report or during any Chapter II procedure.

| Patent document cited in search report | | Publication date | Patent family member(s) | | Publication date |
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| WO 9640885 | A | 19-12-1996 | US 5744346 A | | 28-04-1998 |
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| | | | AU 3075099 A | | 11-10-1999 |
| | | | WO 9947677 A | | 23-09-1999 |
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| | | | EP 1032667 A | | 06-09-2000 |
| | | | WO 9927098 A | | 03-06-1999 |
| | | | AU 3757099 A | | 08-11-1999 |
| | | | WO 9954467 A | | 28-10-1999 |
| | | | AU 1070399 A | | 10-05-1999 |
| | | | EP 1025227 A | | 09-08-2000 |
| | | | WO 9920756 A | | 29-04-1999 |

# FIGURE 170A

```
GTCCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCT
GAAGTGGACCAACTAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGG
ACATCTCAGATCGCTTCCAATGAAGATGGCCTTGCCTTGGGGTCCTGCTTGTTTCATAATCA
TCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGGAAGGAGCACGGGGCTGATCAAGC
CATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTTTCTGAATCTA
GCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGG
TGGCTACTTATTTCTTTTAGGGGATTGTCAGGAGGTGACCACTCTCACGGTGAAATACCAAG
TGTCAGAGGAAGTGCCATCTGGTACAGTGATCGGGAAGCTGTCCCAGGAACTGGGCCGGGAG
GAGAGGCGGAGGCAAGCTGGGGCCGCCTTCCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCAT
TCAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCGGCTGGATCGAGAGCAGCTGT
GCCGACAGTGGGATCCCTGCCTGGTTTCCTTTGATGTGCTTGCCACAGGGGATTTGGCTCTG
ATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGA
GCAGGAGCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTC
TTGACCCAGACACAGGCCCTAACACCCTGCACACCTACACTCTGTCTCCCAGTGAGCACTTT
GCCTTGGATGTCATTGTGGGCCCTGATGAGACCAAACATGCAGAACTCATAGTGGTGAAGGA
GCTGGACAGGGAAATCCATTCATTTTTTGATCTGGTGTTAACTGCCTATGACAATGGGAACC
CCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAGCCCT
GCGTTTGCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCT
CATAAAACTGACCGCCACAGACCCTGACCAAGGCCCCAATGGGGAGGTGGAGTTCTTCCTCA
GTAAGCACATGCCTCCAGAGGTGCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTC
ATTCTGCGTCGACCTCTAGACTATGAAAAGAACCCTGCCTACGAGGTGGATGTTCAGGCAAG
GGACCTGGGTCCCAATCCTATCCCAGCCCATTGCAAAGTTCTCATCAAGGTTCTGGATGTCA
ATGACAACATCCCAAGCATCCACGTCACATGGGCCTCCCAGCCATCACTGGTGTCAGAAGCT
CTTCCCAAGGACAGTTTTATTGCTCTTGTCATGGCAGATGACTTGGATTCAGGACACAATGG
TTTGGTCCACTGCTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCA
ACACATACATGTTGCTAACCAATGCCACACTGGACAGAGAGCAGTGGCCCAAATATACCCTC
ACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATCAGCCAAGAAACAGCTCAGCATTCA
GATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAGCAGGTATGAAGTCTCCACGC
GGGAAAACAACTTACCCTCTCTTCACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGC
ATTAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGA
CTCCAACACAGGAGAGGTCACTGCTCAGAGGTCACTGAACTATGAAGAGATGGCCGGCTTTG
AGTTCCAGGTGATCGCAGAGGACAGCGGGCAACCCATGCTTGCATCCAGTGTCTCTGTGTGG
GTCAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGTCCAGCCTGTGCTCAGCGATGG
AAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCCCATCGAGA
CTCCCAATGGCTTGGGCCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGG
CCATTCCTTTTGACAACCATTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCT
CTACAGCATCCGCAATGGAAATGAAGCCCACCTCTTCATCCTCAACCCTCATACGGGGCAGC
TGTTCGTCAATGTCACCAATGCCAGCAGCCTCATTGGGAGTGAGTGGGAGCTGGAGATAGTA
GTAGAGGACCAGGGAAGCCCCCCCTTACAGACCCGAGCCCTGTTGAGGGTCATGTTTGTCAC
CAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTCGATGCTGA
CGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTCATGTCC
ATCTGCCGGACAGAAAAGAAGGACAACAGGGCCTACAACTGTCGGGAGGCCGAGTCCACCTA
CCGCCAGCAGCCCAAGAGGCCCAGAAACACATTCAGAAGGCAGACATCCACCTCGTGCCTG
TGCTCAGGGGTCAGGCAGGTGAGCCTTGTGAAGTCGGGCAGTCCCACAAAGATGTGGACAAG
GAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTTCCACCTCACCCCGAC
CCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGTGC
TGCAAGACACGGTCAACCTCCTTTTCAACCATCCCAGGCAGAGGAATGCCTCCCGGGAGAAC
CTGAACCTTCCCGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTTGC
AGGCAGCCCCACAGGGAGGCTGGCTGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCAC
CAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCTCAATGGCAAAGTGTCCCCTGAGAAA
GCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTCAGCAAATCTCCCAGCTGC
TGTCCTTGCTGCATCAGGGCCAATTCCAGCCCAAACCAAACCACCGAGGAAATAAGTACTTG
GCCAAGCCAGGAGGCAGCAGGAGTGCAATCCCAGACACAGATGGCCCAAGTGCAAGGGCTGG
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# FIGURE 170B

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AGGCCAGACAGACCCAGAACAGGAGGAAGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGA
AGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCCCAGCACAGGTCTGGCCCTGGAC
CGGCTGAGCGCCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCCTCACCACCAACTA
CCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGT
TCGGCAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTC
TCGGAGATGAGCTCACTGCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGC
CGCCTCCGAGGCGCTGCGGCGGCTCTCGGTCTGCGGGAGGACCCTCAGTTTAGACTTGGCCA
CCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGGAAAGACGGGGACTGAGGGC
AAGAGCAGAGGCAGCAGCAGCAGCAGCAGGTGCCTGTGAACATACCTCAGACGCCTCTGGAT
CCAAGAACCAGGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACTCAC
TAGCTAGCGGCGGCCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAG
CCCCAGGACTAACAGCTGACTGACCAAAGCAGCCCCTTGTAAGCAGCTCTGAGTCTTTTGGA
GGACAGGGACGGTTTGTGGCTGAGATAAGTGTTTCCTGGCAAAACATATGTGGAGCACAAAG
GGTCAGTCCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGGAAAGGGTGGCCTTCTT
GGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTATCAA
TAAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAAA
```

# FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCAGTCCCGGCTGCAGCACCTGGGAGAAGG

CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG

GCAGGAGCCTTCCTTACACTTCGCC**ATG**AGTTTCCTCATCGACTCCAGCATCATGATTACCT

CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT

GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT

GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT

GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTCATGGTGCCTTTTTACATTGGC

TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCCTGTCTCTT

ATGGCTGACCTTTATGTATTTCTTCTGGAAACTAGGAGATCCCTTTCCCATTCTCAGCCCAA

AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAGTGACTCTC

ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT

CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA

TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA

GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG

AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC

TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC

AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT

CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCA

TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT

TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC

CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC

AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA

TACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT

TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC

AGGCACCAGAGAAGCAAATGGCACCT**TGA**ACTTAAGCCTACTACAGACTGTTAGAGGCCAGT

GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC

AAACAAAATGCTATGGTAGCATTTTTCACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA

CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA

GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAAACTAA

AGGTGAAAAATACACTGGAACTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT

AGGATTTCCGTTTTAAGGTTCACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT

AAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG

ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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# FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPFPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISS
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP


**Important features:**

**Signal peptide:**

amino acids 1-23


**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444


**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246


**Eukaryotic cobalamin-binding proteins**

amino acids 151-160


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# FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA

TCATGATTACCTCCCNGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT

TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT

CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT

TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT

TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT

CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

# FIGURE 175

```
GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCTC
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# FIGURE 176A

```
CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGA
TTTGCTACCTTTTTGGCTCCCTGCTCGTCGAACTGCTCTTCTCACGGGCTGTCGCCTTCAAT
CTGGACGTGATGGGTGCCTTGCGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGT
GGCCCTGCACCGGCAGTTGCAGCCCCGACCCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGG
CCCTGGCTCTTCCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGC
CTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAG
CAAGGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCCTGGGGGCAAGATTGTTA
CCTGTGCACACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATG
ATTGGTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGA
ATGGAAGTTCTGTGAGGGACGCCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCA
CAGCTGCCGCCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAAT
TGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGA
CGACGGTCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCCTCATCCCGGTCCCTG
CCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCGTGCAGAAGAGCTG
AGCTTTGTGGCTGGAGCCCCCGCGCCAACCACAAGGGTGCTGTGGTCATCCTGCGCAAGGA
CAGCGCCAGTCGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTG
GCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCC
CCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGCTGTGTATGTGTACTTGAACCAGGG
GGGTCACTGGGCTGGGATCTCCCCTCTCCGGCTCTGCGGCTCCCCTGACTCCATGTTCGGGA
TCAGCCTGGCTGTCCTGGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCC
CCCTTTGATGGTGATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGGTTGTCGCCAA
ACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTCAG
GCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACACC
GCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACG
AAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG
TCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTG
TTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCCGTGTGACGTTCCTGAGCCG
TAACCTGGAAGAACCCAAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCACCAGCATGACC
GAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATT
GTAGTGACCTTGTCCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGG
GCTGCCTCCAGTGGCCCCCATCCTCAATGCCCACCAGCCCAGCACCCAGCGGGCAGAGATCC
ACTTCCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAC
GCCCGCTTCTGTACCCGGGTCAGCGACACGGAATTCCAACCTCTGCCCATGGATGTGGATGG
AACAACAGCCCTGTTTGCACTGAGTGGGCAGCCAGTCATTGGCCTGGAGCTGATGGTCACCA
ACCTGCCATCGGACCCAGCCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTC
CTGGTCATGCTTCCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAA
GCCACTCTGCCTGTCCAATGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGA
AGAGAGGTGCCCAGGTCACCTTCTACCTCATCCTTAGCACCTCCGGGATCAGCATTGAGACC
ACGGAACTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTC
TGCACGAGCCCGTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCCCCAGC
AACTCTTCTTCTCTGGTGTGGTGAGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGC
AGCAAGGTCAAGTATGAGGTCACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTC
TGCCTTCCTCAACATCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAA
TGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCTGGGCAGAAAGGGCTTTGCTCTCCCAGGCCC
AACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGCGGGAGCTGGAGCCACCTGA
GCAGCAGGAGCCTGGTGAGCGGCAGGAGCCCAGCATGTCCTGGTGGCCAGTGTCCTCTGCTG
AGAAGAAGAAAAACATCACCCTGGACTGCGCCCGGGGCACGGCCAACTGTGTGGTGTTCAGC
CACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCA
CAGTGAAGTCCTCCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTGATCCCAGTGATG
GTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTCATCCTCCTGGC
TGTACTGGCTGGGCTGCTGGTGCTAGCACTGCTGGTGCTGCTCCTGTGGAAGATGGGATTCT
TCAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCCTCGG
GAAGACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACTGGGGCAG
```

# FIGURE 176B

```
CCCCCGGCGGGAGGGCCCGGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGG
GCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCCCATGTCCCAGCCTGGCCTGTGG
CTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTG
GTGTCGCATCAAGATTTGGCAGGATCGGCTTCCTCAGGGGCACAGACCTCTCCCACCCACAA
GAACTCCTCCCACCCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGAC
AGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCCTGATGCAAAGGTGGGGAGAAGGGAT
CCTAATCCCTTCCTCTCCCATTCACCCTGTGTAACAGGACCCCAAGGACCTGCCTCCCCGGA
AGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCT
AGTTTCCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTC
TATTTATTAAAAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAA
```

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# FIGURE 177

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
```

```
MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDGGEWKFCEG
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGWPDLIVGAPYFFERQEELGGAVYVYLNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDLNQDGFPDIAVGAPFDGDGKVFIYHGSSLGVVAKPSQVLE
GEAVGIKSFGYSLSGSLDMDGNQYPDLLVGSLADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPSTQRAEIHFLKQGCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
ENASHVECELGNPMKRGAQVTFYLILSTSGISIETTELEVELLLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGQSLRTLGSAFLNIM
WPHEIANGKWLLYPMQVELEGGQGPGQKGLCSPRPNILHLDVDSRDRRRRELEPPEQQEPGE
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRAAVHVWGRLWNSTFLEEY
SAVKSLEVIVRANITVKSSIKNLMLRDASTVIPVMVYLDPMAVVAEGVPWWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGSPRREGP
DAHPILAADGHPELGPDGHPGPGTA
```

**Important features:**

**Signal peptide:**

amino acids 1-33


**Transmembrane domain:**

amino acids 1039-1064


**N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008


**Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-
407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408
and 1031-1047

# FIGURE 178

```
CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCGGACGGCGGTAATTTTC
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAACAGACTTGATACAAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTTGCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAG
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAA
```

# FIGURE 179

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAAWCSQSLAAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFDQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLLRPERSRFDTSILPI
CKDSLGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYYKPTQCHGSVGQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI
```

**Important features:**

**Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

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# FIGURE 180A

```
CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAA
CAGTACCTGACGCCTCTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGC
TGCCCTTCCCCGTGCTCCTTCTGGCCGCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCCGGC
TTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTTCCCGCCGGCCAGAAGGAGTGCTT
CTACCAGCCCATGCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTAGATGGAGCAG
GATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGA
AAATCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAA
TACATTCAGCACCATTTCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAG
AACAGGCACAAGAACAAGAAGATTGGAAGAAATATATTACTGGCACAGATATATTGGATATG
AAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCCAGACTAAGCAAAAGTGGGCA
CATACAAATTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGCAACTTTG
ATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTCAGCCATTCAA
GTTTATATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAAACTCCAAACT
AGAGTACGTAACATTGAAAAATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCAT
TAATGGTCTTCTCCAAAATATTTTGAGATATAAAAGTAGGAAACAGGTATAATTTTAATGTG
AAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAGTTGTACTTAAGTGTGTA
ACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCATTTTC
CTAACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAAT
TGCAACACCAGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTTGTAAATGCGGCAGT
TACAAATTAACTGTGGAAGTTTTCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGA
TGGATTGAATAAATCTTTAGACTACAAAGCCCAACTTTTCTCTATTTACATATGCATCTCT
CCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTGAGATTTTTATAACC
AAATACATTTCAGTGTAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTCC
CAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACAT
GTTTTCTCTTTGAAATGAAGAATATAGTTTAAAAGCTTCCTCCTCCATAGGGACACATTTTC
TCTAACCCTTAACTAAAGTGTAGGATTTTAAAATTAAATGTGAGGTAAAATAAGTTTATTTT
TAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAATAATCATGTTATGTTAATTTTAAC
ATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATATTGCTAAAATG
ATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGG
AAAGAATTTAGAAAAACTTGAGAAAACCTAATCCAAAATAAAATTCACTTAAGTAGAACTAT
AAATAAATATCTAGAATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGG
AGATGATTAATTTCCAGTTAGCTGGAAGAAACTTTGGCTGTAGGTTTTTATTTTCTACAAGA
ATTCTGGTTTGAATTATTTTTGTAAGCAGGTACATTTTATAAAATGTAAGCCCTACTGTAAG
GTTTAGCACTGGGTGTACATATTTATTAAAAATTTTTATTATAACAACTTTTATTAAAATGG
CCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTT
TTAAACACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGA
AGTCTATGGGGGTCTTACTCAAGTACTAGTAATTTAACTTCATCATGAATGAACTATAATTT
TTAAGTTATGCCCATTTATAACGTTGTTTATGACTACATTGTGAGTTAGAAACAAACTTAAA
ATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATTCTTGATGAGCAATAATGA
TAACCAGAGAGTGATTTCATTTACACTCATAGTAGTATAAAAAGAGATACATTTCCCTCTTA
GGCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAA
TGCCGTATATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCC
TCTGCAACACTTGCAGAACAAAGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTG
CGCTGTTAAATTTGCAATGAGAAGCAAATTTACAGTACCATAACTAATAAAGCAGGGTACAG
ATATAAACTACTGCATCTTTTCTATAAAACTGTGATTAAGAATTCTACCTCTCCTGTATGGC
TGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCTAC
ATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTCTTACCATATAAAAAC
GATAATTGCTTTATTTGGAAAGAATTTAGGAATACTAAGGACAATTATTTTTATAGACAAA
GTAAAAGACAGATATTTAAGAGGCATAACCAAAAAGCAAAACTTGTAAACAGAGTAAAAA
TCTTTAATATTTCTAAAGACATACTGTTTATCTGCTTCATATGCTTTTTTTAATTTCACTAT
TCCATTTCTAAATTAAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTTAACAGCTCATTT
TGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTT
CCATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCA
TTTGGATGATTAATGTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGTGTTTGTA
```

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# FIGURE 180B

```
ATTTTATGGTAAAATTAATCCTTCTTACACATAATGGTGTCTTAAAATTGACAAAAAATGAG
CACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTATGTGAAATTTTAAAAGACATTGA
TTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTGCTCAAACTG
CTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATA
ATAAAAATTATCAAAGGAAAA
```

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# FIGURE 181

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
><subunit 1 of 1, 229 aa, 1 stop
><MW: 26017, pI: 4.73, NX(S/T): 0
MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCFDNTFSTISEKVIFFEL
ILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT
```

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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# FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACT**ATG**CTGCCTCCCATGGCCCTGCCCAGTGTGTCCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGAC**TAG**GGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAAACTGCCCTACCTGACTACCTTGTCATGATCCTCC
TTCTTTTTCCTTTTTCTTCACCTTCATTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAAA

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# FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD


Important features:

Signal peptide:

amino acids 1-26


C-type lectin domain signature.

amino acids 146-171

# FIGURE 184

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACC**ATG**CGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTG**TAG**AGTCCCCGCCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAA

# FIGURE 185

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405
<subunit 1 of 1, 125 aa, 1 stop
<MW: 13115, pI: 5.90, NX(S/T): 1
MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL
```

**Important features:**

**Signal peptide:**

amino acids 1-17


**N-glycosylation site.**

amino acids 46-49

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# FIGURE 186

```
CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT .
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTCGCGATGG
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTCAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACTCCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCCTCTTGTTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAAAAAAAAAA
```

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# FIGURE 187

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530
<subunit 1 of 1, 266 aa, 1 stop
<MW: 28672, pI: 8.85, NX(S/T): 1
MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH
```

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

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# FIGURE 188

```
TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG
```

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# FIGURE 189A

```
GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATC
CCGTGCGCCGCGGCTGGGCCGTCGGAGAGTGCGTGTGCTTCTCTCCTGCACGCGGTGCTTGG
GCTCGGCCAGGCGGGGTCCGCCGCCAGGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGAC
CCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGAAGTATTAGAAATGAGCTGAAGAC
CATTCACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTCACCCTTGAAGTAATG
TAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTT
CACTTAAATCAGAACTTGCATAAGAAAGAGA**ATG**GGAGTCTGGTTAAATAAAGATGACTATA
TCAGAGACTTGAAAAGGATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGC
ACAGATCAGGATTTTTACAGTTTACTTGGAGTGTCCAAAACTGCAAGCAGTAGAGAAATAAG
ACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAAAAACCCGAATAACCCAAATG
CACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGATCTACGG
AAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAG
CTGGAACTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGG
AAAGAAGAGAATTTGATGCTGCTGTTAATTCTGGAGAACTGTGGTTTGTAAATTTTACTCC
CCAGGCTGTTCACACTGCCATGATTTAGCTCCCACATGGAGAGACTTTGCTAAAGAAGTGGA
TGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAATGCTTTGCCGAATGAAAG
GAGTCAACAGCTATCCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATATCAT
GGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGAC
AGAACTTTGGACAGGAAATTTTGTCAACTCCATACAAACTGCTTTTGCTGCTGGTATTGGCT
GGCTGATCACTTTTTGTTCAAAAGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTT
AGTGGCATGTTGTTTCTCAACTCATTGGATGCTAAAGAAATATATTTGGAAGTAATACATAA
TCTTCCAGATTTTGAACTACTTTCGGCAAACACACTAGAGGATCGTTTGGCTCATCATCGGT
GGCTGTTATTTTTTCATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAACTA
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCCTCTGCACCAGA
CATCTGTAGTAATCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCA
AAGAATATGAAATTCATCATGGAAAGAAGATTCTATATGATATACTTGCCTTTGCCAAAGAA
AGTGTGAATTCTCATGTTACCACGCTTGGACCTCAAAATTTTCCTGCCAATGACAAAGAACC
ATGGCTTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACTACCAGAGTTAC
GAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCAT
GAGGGACTCTGTAACATGTATAACATTCAGGCTTATCCAACAACAGTGGTATTCAACCAGTC
CAACATTCATGAGTATGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATC
TTATGAATCCTTCAGTGGTCTCCCTTACACCCACCACCTTCAACGAACTAGTTACACAAAGA
AAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTGGTGTCATCCTTGCCAAGTCTT
AATGCCAGAATGGAAAAGAATGGCCCGGACATTAACTGGACTGATCAACGTGGGCAGTATAG
ATTGCCAACAGTATCATTCTTTTTGTGCCCAGGAAAACGTTCAAAGATACCCTGAGATAAGA
TTTTTTCCCCAAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGA
TGCTTATTCCCTGAGAATCTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACAC
CTCAGACTTTCAGTGAAAAAGTTCTACAAGGGAAAAATCATTGGGTGATTGATTTCTATGCT
CCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCTCTTGGCTAGGATGATTAA
AGGAAAAGTGAAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAAAGCTG
GGATCAGGGCCTATCCAACTGTTAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAA
GAAGAGCAGATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATTGGA
AACTCTCCGAAATCAAGGCAAGAGGAATAAGGATGAACTT**TGA**TAATGTTGAAGATGAAGAA
AAAGTTTAAAAGAAATTCTGACAGATGACATCAGAAGACACCTATTTAGAATGTTACATTTA
TGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCAGAATTATCTACAGCA
CTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTAGA
CTTTGCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTT
TGTTATTTGCTTTTAACAACCTTTAAAAAATATTAAAACGATTCTTAGCTCAGAGCCATACA
AAAGTAGGCTGGATTCAGTCCATGGACCATAGATTGCTGTCCCCCTCGACGGACTTATAATG
TTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCTATCTACATAAATGTCTAAGTTGTAT
AAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAACTTAGTTTTTGGTC
ACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTCGTTTTAAAAACACCCA
TGATGTGGCACAGTAAACAAACCCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTT
TTCTTTCCTTCTCAAAGGTTGAAAAAATGCTTTTAATTTTTCACAGCCGAGAAACAGTGCAG
```

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# FIGURE 189B

```
CAGTATATGTGCACACAGTAAGTACACAAATTTGAGCAACAGTAAGTGCACAAATTCTGTAG
TTTGCTGTATCATCCAGGAAAACCTGAGGGAAAAAAATTATAGCAATTAACTGGGCATTGTA
GAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATATGTGTTCAT
GTATTTTCTGAAATTGCTTTCATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTA
ATATTTACATATTTGCCTTCTGAACTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTT
TTCTTTCATAGTTTTGGTTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAAT
TACTTTACAGGTTGTTTTACTGTAGCTTATAATGATACTGTAGTTATTCCAGTTACTAGTTT
ACTGTCAGAGGGCTGCCTTTTTCAGATAAATATTGACATAATAACTGAAGTTATTTTTATAA
GAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGACTCAAA
GAATCACAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGT
AAAAATTCCAATCAGTCAAAAGAGGTCAATGAATTAAAAGGCTTGCAACTTTTTCAAAAAAA
AAAAAAAAAA
```

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# FIGURE 190

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439
<subunit 1 of 1, 747 aa, 1 stop
<MW: 86127, pI: 7.46, NX(S/T): 2
MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYYRYDFGI
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP
SLAVFKGQGTKEYEIHHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIHEYEGHHS
AEQILEFIEDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPEFELLARMIKGKVKAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL
```

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

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# FIGURE 191

```
AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA
GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTGTGAATACTGGGTTCACCA
AAAATCCAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTCACATTTTT
TCAGTCCTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCCTT
TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCCTCTATATTTCCTCCCTTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA
```

# FIGURE 192

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409
<subunit 1 of 1, 300 aa, 1 stop
<MW: 33655, pI: 9.31, NX(S/T): 1
MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAAECRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDVTIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLID
GILTNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK
```

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

# FIGURE 193

```
CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCGCCCGGGGC
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT
CTAGGCCGCACACGGGGCCGCCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGCACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTCAGGTATTTAATACGA
```

# FIGURE 194

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112
<subunit 1 of 1, 414 aa, 1 stop
<MW: 48414, pI: 9.54, NX(S/T): 4
MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTA
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLS
GSLLHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD
```

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

# FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGG**ATG**GCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGCCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCCTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCC**TGA**TTTCTCTCATTT
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTCACCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

# FIGURE 196

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045
<subunit 1 of 1, 270 aa, 1 stop
<MW: 28317, pI: 6.00, NX(S/T): 1
MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLDCVVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG
AELGYGCKASRSTPVDAPDIPS
```

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

# FIGURE 197

```
AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTG
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCCTGTGCGCCGCCG
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG
```

# FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCL
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20


**N-glycosylation site.**

amino acids 75-78


**Homologous region to IL-17**

amino acids 96-180.

# FIGURE 199

```
GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG
GCCGCTTCTTTGTCACCACTCTCCCAGCATTTTTTCATGCAAAGGATGGGATATTCCGCCGT
TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTCACAGTGACTCTTGGAATT
CCTGCTTGGTGTTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAACAAAGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC
TGACACAGAGGTGGTGGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAATCCTTAATTTTTCCTGAATGAGCAAGCTTCTCTTAAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAATCAGGATATAGAAAAACAAACGTAGTGTTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAAATTGTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAATAACTAAAAACCACTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAAA
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTTCCATCTTCTGTAATC
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT
```

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# FIGURE 200

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433
<subunit 1 of 1, 349 aa, 1 stop
<MW: 38952, pI: 4.34, NX(S/T): 1
MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPSCQQTDSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEEEEDNLAAGVDEERSEANDQGPPGEDGVTRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL
```

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.**   (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

# FIGURE 201

```
ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATTCAGGGGCTCTCAAGAACAATGGAATATCATCCTGATTTAGAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTCAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATTCACGTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG
TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTCGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTTTTGAGATAGGGTCT
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAACGG
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
TGTATAATATGTAATTGTAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTAAATACA
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAAACTATATTTCCTCATG
TGCTGATTTGTCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTACAGTCCTCTAATGTTGATTAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTCAT
TTCAATAAAAAAAAACTCTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

# FIGURE 202

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSCAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM
```

**Important features:**

**Type II transmembrane domain:**

amino acids 45-65

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

**N-myristoylation sites.**

amino acids 35-40 and 151-156

**Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

# FIGURE 203A

```
GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGG
TCTCGCTCTGTCACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACC
TCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGAC
TTCCAAGAGTGACTCCGTCGGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACGACACTGTT
CCTGCTGAGTCTGCTCTTCCTGGTCCAAGGTGCCCACGGCAGGGGCCACAGGGAAGACTTTC
GCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGAC
CTGCGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCTTTCCCTGCAGC
CCACCCTGCTTCCCGATCCTTCCCTGACCCCAGGGGCCTCTACCACTTCTGCCTCTACTGGA
ACCGACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAA
GCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTGGCTCAGGGCCCCCGCTGTT
AGCCACTTCTGTCACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCCAGTGCCGCCAGCT
TCACCTTCTCCTTCCACAGTCCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGC
GAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCTCAAG
GAGGCCCTCGGCTGCCCCCGCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTG
TGAGATTCATGGGGGACATGGTGTCCTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAG
CTCCAGCCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGGCAGGAGGAGGAGCAGAG
CGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGCCGGA
GCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGAC
AAGAATTCCAGCCAAGTCCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGT
AGCCAACCTCACGGAGCCCGTGGTGCTCACTTTCCAGCACCAGCTACAGCCGAAGAATGTGA
CTCTGCAATGTGTGTTCTGGGTTGAAGACCCCACATTGAGCAGCCCGGGGCATTGGAGCAGT
GCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGCAACCACTTGACCTA
CTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGCC
TCCTCTCCTACGTGGGCTGTGTCGTCTCTGCCCTGGCCTGCCTTGTCACCATTGCCGCCTAC
CTCTGCTCCAGGGTGCCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCA
CATGAACCTGCTGCTGGCCGTCTTCCTGCTGGACACGAGCTTCCTGCTCAGCGAGCCGGTGG
CCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCCATCTTCCTGCACTTCTCCCTGCTC
ACCTGCCTTTCCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACTCGTGGTGGAGGTCTT
TGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCT
TTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACTATGGCCCCATCATCTTGGCTGTG
CATAGGACTCCAGAGGGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAG
CTACATCACCAACCTGGGCCTCTTCAGCCTGGTGTTTCTGTTCAACATGGCCATGCTAGCCA
CCATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAAAAGTGGTCACATGTGCTGACA
CTGCTGGGCCTCAGCCTGGTCCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCCTTTGCTTC
TGGCACCTTCCAGCTTGTCGTCCTCTACCTTTTCAGCATCATCACCTCCTTCCAAGGCTTCC
TCATCTTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCTCCCCTCTGAAG
GGCCTCCAGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCCTGT
GGCCCCCGAGCCAGGCCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGAAAGCCCAACGACC
ATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTGGCCTT
GGGGACTACTCGGCTCTCACTCAGCTCCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTA
GGGTACTGTCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTG
GGCCCAGCCCTCATTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATC
CTGTGCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCACCCTGA
GGGCACTCTGCATCCTCTGTCATTTTAACCTCAGGTGGCACCCAGGGCGAATGGGGCCCAGG
CTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCCCTCAGCCCCCCAGTCCTCCCTCCATCTT
CCCTGGGGTTCTCCTCCTCTCCCAGGGCCTCCTTGCTCCTTCGTTCACAGCTGGGGGTCCCC
GATTCCAATGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGT
TTGTCTACTGCACAAGCCTCGGCCTGCCCCTGAGCCAGGCTCGGTACCGATGCGTGGGCTGG
GCTAGGTCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTGCTCACCCTGACC
AAGCACACGCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAACTGTGG
ACCATGCCAGTCCCGTCTGGTTTCCATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTG
GTGACACTGGCCTAGAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAAATAGCTC
```

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# FIGURE 203B

```
CAGGCGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAACACACACGGGTAGATTGC
TGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCCTCCTGCCAACATTC
AGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAACTCCTGGAGCTACAGGGACAGGGAGCCAT
CATTCCTGCCTGGGAATCCTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGA
AGATGGGAAGGATGTTCTTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTA
CATGTTCATTGTAGAGAATTTGGAAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAATCAG
CTGTTGTAATCGCCTAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

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# FIGURE 204

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921
<subunit 1 of 1, 693 aa, 1 stop
<MW: 77738, pI: 8.87, NX(S/T): 7
MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPPHTAAHNASVDMCELKRDLQLL
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTLFQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLTFQHQLQPKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRVPLPC
RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI
```

**Important features:**

**Signal peptide:**

amino acids 1-25


**Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657


**Microbodies C-terminal targeting signal.**

amino acids 691-693


**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373


**N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344


**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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# FIGURE 205

```
TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTTCTGTTCAACATGG
```

# FIGURE 206

```
CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCA
GGTTTTGCTTTGATCCTTTTCAAAAACTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTT
GGATGGGATTATGTGGAAACTACCCTGCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCC
ACCCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGACTCGGGAGTCGCTGCTTCCAAAGT
GCCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGCT
GACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAAT
TCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATT
ACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATAC
GGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTACGTTTGATG
AAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAG
GAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAAACA
GATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAAC
CAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCA
GTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTAC
CTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTAT
ATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTGGAAGAAAATCCAGAGTGGTG
GATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGT
GTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTA
AACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCA
AGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGG
ATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCA
GAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGC
AGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTT
CAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATT
AGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATC
GTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTA
CGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGT
ACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCC
ATGTCCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGCTCATATTCAC
ATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCT
ATGAATTAAACTTGTGTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAAT
TTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAG
AGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTAT
ATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTAC
CAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATT
TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGAC
AAAAATACATGTATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAA
CTGAATTGGAATAGAATTGGTAAGTTGCAAGACTTTTTGAAAATAATTAAATTATCATATC
TTCCATTCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATTCAGATCC
AGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGC
ACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACAT
CCTATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAAT
ACATGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCA
ATTTAAAAGAAAATCAGTAAAATATTTTGCTTGTAAAATGCTTAATATNGTGCCTAGGTTAT
GTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAAGAATGTGGCTATTTTGG
GGAGAAAATTAAAAAAAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC
```

# FIGURE 207

```
MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
```

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# FIGURE 208

```
CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATT
CCATTTTGGAAGAAGACTAAAAATGGTGTTTCCAATGTGGACACTGAAGAGACAAATTCTTA
TCCTTTTTAACATAATCCTAATTTCCAAACTCCTTGGGGCTAGATGGTTTCCTAAAACTCTG
CCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTGATCGTGGACTGCACAGACAAGCA
TTTGACAGAAATTCCTGGAGGTATTCCCACGAACACCACGAACCTCACCCTCACCATTAACC
ACATACCAGACATCTCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTC
AGATGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCA
GATTAAACCCAGAAGCTTTAGTGGACTCACTTATTTAAAATCCCTTTACCTGGATGGAAACC
AGCTACTAGAGATACCGCAGGGCCTCCCGCCTAGCTTACAGCTTCTCAGCCTTGAGGCCAAC
AACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCCAACATAGAAATACTCTACCT
GGGCCAAAACTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAAGATGCCT
TCCTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCCT
ACTGTTTTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCA
AGAAGATGATTTTAATAACCTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTC
GTTGTTATAATGCCCCATTTCCTTGTGCGCCGTGTAAAAATAATTCTCCCCTACAGATCCCT
GTAAATGCTTTTGATGCGCTGACAGAATTAAAAGTTTTACGTCTACACAGTAACTCTCTTCA
GCATGTGCCCCCAAGATGGTTTAAGAACATCAACAAACTCCAGGAACTGGATCTGTCCCAAA
ACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAA
TTGGATCTGTCTTTCAATTTTGAACTTCAGGTCTATCGTGCATCTATGAATCTATCACAAGC
ATTTTCTTCACTGAAAAGCCTGAAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGA
AAAGCTTTAACCTCTCGCCATTACATAATCTTCAAAATCTTGAAGTTCTTGATCTTGGCACT
AACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGACTGAAAGTCATAGA
TCTTTCAGTGAATAAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAATG
CCAGAACTTCTGTAGAAAGTTATGAACCCCAGGTCCTGGAACAATTACATTATTTCAGATAT
GATAAGTATGCAAGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGA
AAGCTGCTACAAGTATGGGCAGACCTTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGT
CCTCTGATTTTCAGCATCTTTCTTTCCTCAAATGCCTGAATCTGTCAGGAAATCTCATTAGC
CAAACTCTTAATGGCAGTGAATTCCAACCTTTAGCAGAGCTGAGATATTTGGACTTCTCCAA
CAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAAACTGGAAGTTCTGG
ATATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACC
AAGAACCTAAAGGTTCTGCAGAAACTGATGATGAACGACAATGACATCTCTTCCTCCACCAG
CAGGACCATGGAGAGTGAGTCTCTTAGAACTCTGGAATTCAGAGGAAATCACTTAGATGTTT
TATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAGAATCTGCTAAAATTAGAGGAA
TTAGACATCTCTAAAAATTCCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGTATGCCTCC
AAATCTAAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAAACTCC
AGTGTCTAAAGAACCTGGAAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAG
AGATTATCCAACTGTTCCAGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAG
TCTGACGAAGTATTTTCTACAAGATGCCTTCCAGTTGCGATATCTGGATCTCAGCTCAAATA
AAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTCAACAATCTGAAGATGTTG
CTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGGGTTAA
CCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCAC
ACAAGGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG
ATTCTGTTCTCACTTTCCATATCTGTATCTCTCTTTCTCATGGTGATGATGACAGCAAGTCA
CCTCTATTTCTGGGATGTGTGGTATATTTACCATTTCTGTAAGGCCAAGATAAAGGGGTATC
AGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTATGACACTAAAGACCCA
GCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAAACTGGAAGACCCAAGAGAGAAACA
TTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTT
CCCAGAGCATACAGCTTAGCAAAAAGACAGTGTTTGTGATGACAGACAAGTATGCAAAGACT
GAAAATTTTAAGATAGCATTTTACTTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGT
GATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAGTCCAAGTTCCTCCAGCTCCGGAAAA
GGCTCTGTGGGAGTTCTGTCCTTGAGTGGCCAACAAACCCGCAAGCTCACCCATACTTCTGG
CAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGA
AACGGTCTAGCCCTTCTTTGCAAAACACAACTGCCTAGTTTACCAAGGAGAGGCCTGGC
```

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# FIGURE 209

```
MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYYR
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIP
YLATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLCLEE
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLKNALATDNHVAYSQVFKETV
```

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# FIGURE 210A

```
GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAA
AACATGTTCCTTCAGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGGTTCCTGTGA
GTTATGCGCCGAAGAAAATTTTTCTAGAAGCTATCCTTGTGATGAGAAAAGCAAAATGACT
GTGACAGAACTAGACCTGTCTGATAATTTCATCACACACATAACGAATGAATCATTTCAAGG
GCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAA
ATCCCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCCTCAACCTAAAAAAC
CTAAGGGAGTTACTGCTTGAAGACAACCAGTTACCCCAAATACCCTCTGGTTTGCCAGAGTC
TTTGACAGAACTTAGTCTAATTCAAAACAATATATACAACATAACTAAAGAGGGCATTTCAA
GACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAACTGCTATTTTAACAAAGTTTGCGAG
AAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTATCACTATC
TTTCAATTCTCTTTCACACGTGCCACCCAAACTGCCAAGCTCCCTACGCAAACTTTTTCTGA
GCAACACCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTA
CTAGATTTAAGCGGGAACTGTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCCTTGTGA
TGGTGGTGCTTCAATTAATATAGATCGTTTTGCTTTTCAAAACTTGACCCAACTTCGATACC
TAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGTTTAAAAATATGCCTCAT
CTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCATTTTT
AACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATC
CACAGCATATTAATATTTCCAGAAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTA
AGAGGTTATGTGTTCCAGGAACTCAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAA
CTTATCGACTATCAACTTGGGTATTAATTTTATTAAGCAAATCGATTTCAAACTTTTCCAAA
ATTTCTCCAATCTGGAAATTATTTACTTGTCAGAAAACAGAATATCACCGTTGGTAAAAGAT
ACCCGGCAGAGTTATGCAAATAGTTCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAAC
AGATTTTGAGTTTGACCCACATTCGAACTTTTATCATTTCACCCGTCCTTTAATAAAGCCAC
AATGTGCTGCTTATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCA
AACCAATTTGAAAATCTTCCTGACATTGCCTGTTTAAATCTGTCTGCAAATAGCAATGCTCA
AGTGTTAAGTGGAACTGAATTTTCAGCCATTCCTCATGTCAAATATTTGGATTTGACAAACA
ATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGGAAGTTCTAGAT
CTCAGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCA
AAATTTCACAAATCTAAAAGTTTTAAACTTGAGCCACAACAACATTTATACTTTAACAGATA
AGTATAACCTGGAAAGCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGACATT
TTGTGGAATGATGATGACAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAATCTGACACG
TCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATGAAGCATTCCTTAATTTGCCAG
CGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAACTGGACATTACTC
CAGCAGTTTCCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAAACTACTCTTTTTAACTGA
TAGCCTATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCC
ACCTACCCTCTGGCTTTCTTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAAT
CTGCTAAAAACAATCAACAAATCCGCACTTGAAACTAAGACCACCACCAAATTATCTATGTT
GGAACTACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAGATTTCCGAAGATGGATGG
ATGAACATCTGAATGTCAAAATTCCCAGACTGGTAGATGTCATTTGTGCCAGTCCTGGGGAT
CAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTCAGATGTCACTGCAGT
GATATTATTTTTCTTCACGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACC
ATTTGTTTTACTGGGATGTTTGGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTAC
AGGTCTCTTTCCACATCCCAAACTTTCTATGATGCTTACATTTCTTATGACACCAAAGATGC
CTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAGAGAGCCGAGACAAAA
ACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACCTC
ATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAG
CTGGAACTTTAAAACAGCTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATG
TGATTATATTTATCCTGCTGGAGCCAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAG
CGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTG
GCAAACTCTGAGAAATGTGGTCTTGACTGAAAATGATTCACGGTATAACAATATGTATGTCG
ATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTCGCGCCATAATAAAGATGCAAA
GGAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTATCCCAAAACTTAGTGG
TTTAAAACAACACATTTGCTGGCCCACAGTTTTTGAGGGTCAGGAGTCCAGGCCCAGCATAA
```

# FIGURE 210B

```
CTGGGTCCTCTGCTCAGGGTGTCTCAGAGGCTGCAATGTAGGTGTTCACCAGAGACATAGGC
ATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCAATTCCTCCTGGGCTATTGGCCA
AAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCACAAGGCAGCTTGCTTCATCAGAGCT
AGCAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAATCGAATCAAAAAAG
TGATATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACCAGCT
CCATGGGAGTGACCACCTCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGAT
TGCTTCAGTTGGTCATCAACTATTTTCCCTTGACTGCTGTCCTGGGATGGCCTGCTATCTTG
ATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACCATCTTAGCAGTTGACCTAA
CACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATATTAAGC
TGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTCG
GTTTTATTTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATG
CCATTTAAGAACTGAGATGGATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAA
GTATGCAGCTAAATTCGAAGCTTTTGGTCTATATTGTTAATTGCCATTGCTGTAAATCTTAA
AATGAATGAATAAAAATGTTTCATTTTACAAAAAAAAAAAAAAAAA
```

## FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPQTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQNGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTQLRYLNLSSTSLRKINAAWFKNM
PHLKVLDLEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFSNLEIIYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDLS
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPGLAIID
NLMQSINQSKKTVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNNMYVDSIKQY

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# FIGURE 212

```
CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCCTG
GAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG
GACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT
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# FIGURE 213

```
MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR .
CPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS
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# FIGURE 214

```
GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGCCCGGGGAGGGGAACTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTA·
CCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCG
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAATAAAAATGAAACGTG
```

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# FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

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# FIGURE 216

```
CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCCTGGAGGAGCAGCT
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTG
```

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## FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

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# FIGURE 218

```
GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCTTGTCAGGAGGAGACAGCCTC
CCGGCCCGGGGAGGACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTC
CGTTTCCTGCCGTCAGCTGCCGGCCGAGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTC
CTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGGAGATTGTCTTCCAGGGCTAGCAA
TTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGATTTCAAAGCTG
GGCTCAGCCTCTGTTTCTTCTCGTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCCAA
TCATGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCCAGGCAGG
AACACCTTTTGCTGTGATGGCCGCGTCATGATGGCCCGGCAAAAGGGCATTTTCTACCTGAC
CCTTTTCCTCATCCTGGGGACATGTACACTCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTG
TTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCTTCCTTTTCTCCATGGCTACA
CTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCCTCGGGCGCTACCAGATGAAGCAGC
TTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGC
CTCGTATCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGC
AAGATCTTCCGGCCTCCCCGGGCCTCCCATTGCAGCATCTGTGACAACTGTGTGGAGCGCTT
CGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTACCGCTACTTCTACC
TCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCTTCAACATCGTCTATGTG
GCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAAACTCCTGGAACTGTTCT
AGAAGTCCTCATTTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCATACTT
TCCTCGTGGCTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAAT
CGCGTCCAGAATCCCTACAGCCATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGG
CCCCTTGCCCCCCAGTGTGCTGGATCGAAGGGGTATTTTGCCACTGGAGGAAAGTGGAAGTC
GACCTCCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCCCAGCCCCCACAGAA
CACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAGA
GCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACT
TTTGTTTGTGTTTAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGAG
AGCAAGTAAGCTGTCCCTTTTAACTGTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTG
GCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACTCAAGGCAGTGGCAGAAGATGTCAG
TCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCTCCATGGCCTCA
GCCACAGGGTCCCCTTGGACCCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTC
ACTGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCA
CGTGCTGAGTCCAGAGGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTTCTTGG
GGTCTTCAGGACTGAAGAGGAGGGAGAGTGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCC
AGCATTGCCCACAAATCCTTTTAGGAATGGGACAGGTACCTTCCACTTGTTGTANNNNNNNNN
NNNNNNNNNNNNNNNNNNTTGTTTTTCCTTTTGACTCCTGCTCCCATTAGGAGCAGGAATG
GCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCCTCAGAGGAAGCCCGAGTGCTCACT
TAAACACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGG
AAACCAAGGCACAGAGAGGCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAA
AAAAATGCTAACCAGTTCTTCCATTAAGCCTCGGCTGAGTGAGGGAAAGCCCAGCACTGCTG
CCCTCTCGGGTAACTCACCCTAAGGCCTCGGCCCACCTCTGGCTATGGTAACCACACTGGGG
GCTTCCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTTCACCC
TGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTCAGGGAAGAAG
ATTTATGTATTATATGTGGCTATATTTCCTAGAGCACCTGTGTTTCCTCTTTCTAAGCCAG
GGTCCTGTCTGGATGACTTATGCGGTGGGGGAGTGTAAACCGGAACTTTTCATCTATTTGAA
GGCGATTAAACTGTGTCTAATGCA
```

# FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV.
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL
FILSLSLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLICFFTLWSVVGLTGFHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAEK

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# FIGURE 220

```
AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT
```

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# FIGURE 221

```
GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA
AAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTC
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAGAGCAAAA
AAAAA
```

# FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

# FIGURE 223

GAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT .
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

# FIGURE 224

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ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGCGGCCCGGGAGCGGGCCAGCTG
CCGGGAGCCCTGAATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGG
GAGCTGGCAGCAACGTGGGATTCCAGAAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAG
CTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCTGCACTGCTTCTGGGCTGCCTTGT
GGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACAGAGGCCTGCA
TTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTT
TACCAGTTCTCCTGTGGGGGCTGGATTCGGAGGAACCCCCTGCCCGATGGGCGTTCTCGCTG
GAACACCTTCAACAGCCTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACA
CCACCTTCAACTCCAGCAGTGAAGCTGAGCAGAAGACACAGCGCTTCTACCTATCTTGCCTA
CAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGAGACCTCATTGAGAAGATTGG
TGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACTTTATGGAGGTGTTGAAGGCAGTAG
CAGGGACCTACAGGGCCACCCCATTCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCC
AACAGCAATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTT
AAACAGAACTGCCAATGAGAAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACTGGGGA
TGCTGCTGGGTGGGCGGCCCACCTCCACGAGGGAGCAGATGCAGCAGGTGCTGGAGTTGGAG
ATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGCGACGAGGAGAAGATCTACCA
CAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTCCTGT
CTTTCTTGCTGTCACCATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGAT
TATTTGCAGCAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCT
GATCTGGAACCTGGTGCAAAAGACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAG
AGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAGTCCTGTGTGCCGAGGTGGCAGACCTGC
ATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTCGTGAAGGCCACGTT
TGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAGG
AGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCA
GATGCCATCTATGATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGA
TGTTTATGACGGGTACGAAATTTCTGAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACA
ACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAGCCTCCCAGCCGAGACCAGTGGAGC
ATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACTAAGAATGAGATCGTCTTCCCCGC
TGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCA
TCGGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGAC
AAAGAAGGGAACCTGCGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACAC
GGCCTGCATGGAGGAACAGTACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCC
AGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAA
GCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCA
GCTCTTCTTCGTGGGATTTGCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACG
AGGGGCTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAAC
TCCCGTGACTTCCTGCGGCACTTCGGCTGCCCTGTCGGCTCCCCATGAACCCAGGGCAGCT
GTGTGAGGTGTGGTAGACCTGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCA
GCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGT
CTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCT
CTGCTTTGGGGGTGCCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGT
GTCACCCTGCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC
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# FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSRDYYLNRTANEKVLTAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLLETLYGTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGQLCEVW

# FIGURE 226A

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GCCCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCGCTCCCGCGCCCTCCTC
CCTCCCTCCTCCCCAGCTGTCCCGTTCGCGTCATGCCGAGCCTCCCGGCCCCGCCGGCCCCG
CTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGGCCCGCGGCGCCGGCCCAGAGCC
CCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTCGGGGAGCGGCAGGTAGGT
GGGCGCCCGGGGGAGGCGCGGGCGGGGAGTCGGGCTCGGGGCGAGTCAGCGCCAGCCCGGAG
GGGGCGCGGGGCGCAGGTGGCTCGGCGCGGCGGGCGGCCCGGAGGGTGGGCGGGGGCAGAAG
GGCGCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGGCGGCACACGGCGCGAGCTG
GGCAGCGGCCTCCAGCCAAGCCCGTCCCCGCAGGCTGCACCTTCGGCGGGAAGGTCTATGCC
TTGGACGAGACGTGGCACCCGGACCTAGGGGAGCCATTCGGGGTGATGCGCTGCGTGCTGTG
CGCCTGCGAGGCGCAGTGGGGTCGCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACA
TCAAACCAGAGTGCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGC
CAGACCTGCCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTCGCAGGCGGTGGCACG
AGCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACC
GCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCCTGTTTGAGCACCCTGCAGCC
CCCACCCAAGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCTCGGTTGTCTCTGCGGCT
CCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCACCCTTCAGGGGAGGTCT
GGGGGCCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGACTCTA
GAAGGCCCCACCAGCAGGGCGTAGGGGGCATCACCCTGCTCACTCTCAGTGACACAGAGGA
CTCCTTGCATTTTTTGCTGCTCTTCCGAGGCCTTGCAGGACTAACCCAGGTTCCCTTGAGGC
TCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAA
CCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGG
GGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTG
CTGCCAGGAAGAGCTGCGACGTCCTGCAAAGTGTCCTTTGTGGGGCTAATGCCCTGATCCCA
GTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCCTGATCCT
CCAGGTGCAATTGGTAGGGACAACCAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTC
AGCGGAGGGATCAGCCCACTGTCCTGTGCCACATGGCTGGCCTATCCTCCCCTGCCCCCAGG
CCGTGGGTATCTGCCCTGGGCTGGGGTGCCCGAGGGGCTCATATGCTGCTGCAGAATGAGCT
CTTCCTGAACGTGGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCAACGTGGCTGCC
CTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTGCCCCTAGCAGGAGCCCTGGTGCTA
CCCCCTGTGAAGAGCCAAGCAGCAGGGCACGCCTGGCTTTCCTTGGATACCCACTGTCACCT
GCACTATGAAGTGCTGCTGGCTGGGCTTGGTGGCTCAGAACAAGGCACTGTCACTGCCCACC
TCCTTGGGCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAG
GCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACTGCTGCGGCACCTGGCAAAAGGCATGGC
TTCCCTGATGATCACCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCTCTCCTCCC
AGGTGCACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCCTGGAGGCGGCCGGGGCCGAG
GGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCCTGTGGTGCCTGGTCT
CCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCCTGGGCGGCCCCGAGACCCCAACACATGCT
TCTTCGAGGGGCAGCAGCGCCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGC
TCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCCACCGCCCAG
CTGCCCACACCCGGTGCAGGCTCCCGACCAGTGCTGCCCTGTTTGCCCTGGCTGCTATTTTG
ATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCCTTTGGC
TTAATTAAGTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAA
AACAGTGTCCAGGTGAGGCCCACCCCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGG
GGCTGCCGTTTTGCTGGGCAGTGGTTCCCAGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCC
GTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGTGT
GAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCCAGGGAGGTCCCTGAAGAA
GCTGAAGGTCACTGTGTCCCAGTGCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACC
AGGCAGGGGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCCTGTGGCTCGGGG
AAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCCACCGGCGGCGTAAGTGAGGGAGTCCAGG
GTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAGGGAAGGGAGCAC
TCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCCTCACAGC
AACCTGGTGGAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGA
AATTAAGCAACGAGATGAAGGTCACCCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGC
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# FIGURE 226B

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CTTTCTGGGACCAAGGCAGGGATGCTTTGCCCTGCCCTCTATGCCTCTCTGTGCCTCTCCAC
TCCCTCTCCCCTCCTCCAACATTCCCTCCCTTCTGTCTCCAGCAGCCCCAGAGACCAGAACT
GATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCCAAGTGACCA
AGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCATTCTCCTGTGG
GAAGCCCAGTGCCTTTGCTCCTCTGTCCTGCCTCTACTCCCACCCCCACTACCTCTGGGAAC
CACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTCACAGCCACTCCAAGTCCT
GCCCTGCCACCCTCGGCCTCTGTCCTGGAAGCCCCACCCCTTTCTTCCTGTACATAATGTCA
CTGGCTTGTTGGGATTTTTAATTTATCTTCACTCAGCACCAAGGGCCCCGGACACTCCACTC
CTGCTGCCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTTGTATTTATTAAAACATTTCT
TTTTCAGTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGG
AGAAGGGGCNGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGA
CCTGGAGAGGCAGAGGATAGCGTGGCNNTTGGCTGGCATNCCTGGGTTCCGCAGAGGGGCTG
GGGATGGTTCTTGAGATGGTCTAGAGACTCAAGAATTTAGGGAAGTAGAAGCAGGATTTTGA
CTCAAGTTTAGTTTCCCACATCGCTGGCCTGTTTGCTGACTTCATGTTTGAAGTTGCTCCAG
AGAGAGAATCAAAGGTGTCACCAGCCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTTCTTTC
CCTCCCCTCCCCTCCCCTCCCCTCCCCTCC
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# FIGURE 227

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GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTCGGA
GGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAAACTGCCCCT
CCTTTCTTTCTTCTTTTCTTCCTCCCTCCCTCCCTTTCTTCCCCTTTTCCTTCCTTCCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTCGATGGGTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG
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## FIGURE 228

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ATGCCTACTACCTTCCAACTAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCCT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCCTCACGGGCTACCCCCACCTCACCCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTACAGAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC
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